CLAIMS

1. Method for mass-spectrometric analysis of known mutation sites in genome DNA by mutation-dependent primer extension,
wherein the nucleotide chain of the extension primer contains a photocleavable linker which is cleaved by UV light irradiation before mass spectrometric analysis.

2. Method as in Claim 1, wherein the linker is located 3 to 10 bases from the 3' position of the primer.

3. Method as in Claim 1, wherein the linker is derived from the class of chemical compounds known as o-nitrobenzyl derivatives.

4. Method as in Claim 1, wherein the extension is carried out by using a mixture of four types of nucleoside triphosphate derivative terminators so that extension only takes place by precisely one base.

5. Method as in Claim 4, wherein dideoxynucleoside triphosphates are used as the nucleoside triphosphate derivative terminators.

6. Method as in Claim 1, wherein the extension using a mixture of non-terminating and terminating nucleoside triphosphate derivatives is carried out so as to produce length differences in the extended primers of at least one base depending on mutation.

7. Method as in Claim 1, wherein the internucleotide cyanoethyl phosphite bond of the primer nucleotides between the linker and the 3' position are sulphurized forming phosphorothioate nucleotides, and wherein the phosphorothioate nucleotides are alkylated before analysis by mass spectrometry.

8. Method as in Claim 7, wherein the extension is carried out with a mixture of four types of nucleoside triphosphate derivative terminators and the negatively charged ions are measured in the mass spectrometer.

9. Method as in Claim 8, wherein dideoxynucleoside triphosphates are used as the nucleoside triphosphate derivative terminators.

10. Method as in Claim 9, wherein the extension is carried out with a mixture of four types of nucleoside triphosphate derivative terminators in which the nucleotide which is inserted, like the phosphorothioate nucleotides of the primer, is alkylated before analysis by mass spectrometry and the negative ions are measured in the mass spectrometer.

11. Method as in Claim 10, wherein α-thiodideoxynucleoside triphosphates are used as the nucleoside triphosphate derivative terminators.

12. Method as in Claim 11, wherein each one of the α-thionucleoside triphosphate derivative terminators carries a chemical group with a positive charge in addition.

13. Method as in Claim 10, wherein one of the phosphorothioate nucleotides of the extension primer carries a chemical group with a positive charge.

14. Method as in Claim 13, wherein the chemical group carrying the charge is located on the second, third or fourth nucleobase counting from the 3' position.

15. Method as in Claim 12, wherein the chemical group carrying the charge is a quaternary ammonium group.

16. Method as in Claim 10, wherein the primer for the primer extension carries an anchor for the attachment of a charge group which is attached before the analysis by mass spectrometry is carried out.

17. Method as in Claim 16, wherein the anchor carries a free amino group.

18. Method as in Claim 1, wherein ionization in the mass-spectrometric mass determination is achieved by using matrix-assisted laser desorption and ionization (MALDI).

19. Method as in Claim 12, wherein ionization in the mass-spectrometric mass determination is achieved by using matrix-assisted laser desorption and ionization (MALDI), and wherein a matrix is used which does not contribute to the transfer of charge to the DNA products being measured.

20. Method as in Claim 19, wherein α-cyano-4-hydroxycinnamic acid methyl ester is used as the matrix.

21. Method as in Claim 1, wherein the 5' position of the extension primer is biotinylated.

22. Method as in Claim 21, wherein the primers, after extension, are bonded via biotin to streptavidine molecules which are fixed to a surface for the purpose of purging all the components of the reaction fluid which was required for the extension.

23. Method as in Claim 22, wherein the streptavidine is bonded to the surface of a sample support which is also used for further mass-spectrometric analysis.